

SEQUENCE LISTING

(1) GENERAL INFORMATION:
 (i) APPLICANT: ANDERTON, STEPHEN MARK
 VAN DER ZEE, RUURD
 VAN EDEN, WILLEM
 (ii) TITLE OF INVENTION: PEPTIDE FRAGMENTS OF MICROBIAL STRESS
 PROTEINS AND PHARMACEUTICAL COMPOSITION MADE THEREOF FOR THE
 TREATMENT AND PREVENTION OF INFLAMMATORY DISEASES
 (iii) NUMBER OF SEQUENCES: 6
 (iv) CORRESPONDENCE ADDRESS:
 (A) ADDRESSEE: THE WEBB LAW FIRM
 (B) STREET: 700 KOPPERS BUILDING, 436 SEVENTH AVENUE
 (C) CITY: PITTSBURGH
 (D) STATE: PENNSYLVANIA
 (E) COUNTRY: UNITED STATES OF AMERICA
 (F) ZIP: 15219-1818
 (v) COMPUTER READABLE FORM:
 (A) MEDIUM TYPE: 3.5" FLOPPY DISK
 (B) COMPUTER: Midwest Micro 486-50
 (C) OPERATING SYSTEM: DOS
 (D) SOFTWARE: WORDPERFECT 6.1
 (vi) CURRENT APPLICATION DATA:
 (A) APPLICATION NUMBER: 08/716,169
 (B) FILING DATE: 18-SEP-1996
 (C) CLASSIFICATION:
 (vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: PCT/NL95/00108
 (B) FILING DATE: 21-MAR-1995
 (2) INFORMATION FOR SEQ ID NO: 1:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 540
 (B) TYPE: AMINO ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: UNKNOWN
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Met	Ala	Lys	Thr	Ile	Ala	Tyr	Asp	Glu	Glu	Ala	Arg	Arg	Gly	Leu	15
Glu	Arg	Gly	Leu	Asn	Ala	Leu	Ala	Asp	Ala	Val	Lys	Val	Thr	Leu	30
Gly	Pro	Lys	Gly	Arg	Asn	Val	Val	Leu	Glu	Lys	Lys	Trp	Gly	Ala	45
Pro	Thr	Ile	Thr	Asn	Asp	Gly	Val	Ser	Ile	Ala	Lys	Glu	Ile	Glu	60
Leu	Glu	Asp	Pro	Tyr	Glu	Lys	Ile	Gly	Ala	Glu	Leu	Val	Lys	Glu	75
Val	Ala	Lys	Lys	Thr	Asp	Asp	Val	Ala	Gly	Asp	Gly	Thr	Thr	Thr	90
Ala	Thr	Val	Leu	Ala	Gln	Ala	Leu	Val	Arg	Glu	Gly	Leu	Arg	Asn	105
Val	Ala	Ala	Gly	Ala	Asn	Pro	Leu	Gly	Val	Lys	Arg	Gly	Ile	Glu	120
Lys	Ala	Val	Glu	Lys	Val	Thr	Glu	Thr	Leu	Leu	Lys	Gly	Ala	Lys	135
Glu	Val	Glu	Thr	Lys	Glu	Gln	Ile	Ala	Ala	Thr	Ala	Ala	Ile	Ser	150
Ala	Gly	Asp	Gln	Ser	Ile	Gly	Asp	Leu	Ile	Ala	Glu	Ala	Met	Asp	165
Lys	Val	Gly	Asn	Glu	Gly	Val	Ile	Thr	Val	Glu	Glu	Ser	Asn	Thr	180
Phe	Gly	Leu	Gln	Leu	Glu	Leu	Thr	Glu	Gly	Met	Arg	Phe	Asp	Lys	195
Gly	Tyr	Ile	Ser	Gly	Tyr	Phe	Val	Thr	Asp	Pro	Glu	Arg	Gln	Glu	210
Ala	Val	Leu	Glu	Asp	Pro	Tyr	Ile	Leu	Leu	Val	Ser	Ser	Lys	Val	225
Ser	Thr	Val	Lys	Asp	Leu	Leu	Pro	Leu	Leu	Glu	Lys	Val	Ile	Gly	240
Ala	Gly	Lys	Pro	Leu	Leu	Ile	Ile	Ala	Glu	Asp	Val	Glu	Gly	Glu	255
Ala	Leu	Ser	Thr	Leu	Val	Val	Asn	Lys	Ile	Arg	Gly	Thr	Phe	Lys	270
Ser	Val	Ala	Val	Lys	Ala	Pro	Gly	Phe	Gly	Asp	Arg	Arg	Lys	Ala	285
Met	Leu	Gln	Asp	M t	Ala	Ile	Leu	Thr	Gly	Gly	Gln	Val	Il	Ser	300
Glu	Glu	Val	Gly	Leu	Thr	Leu	Glu	Asn	Ala	Asp	Leu	Ser	Leu	Leu	315

Gly	Lys	Ala	Arg	Lys	Val	Val	Val	Thr	Lys	Asp	Glu	Thr	Thr	Ile	330
Val	Glu	Gly	Ala	Gly	Asp	Thr	Asp	Ala	Ile	Ala	Gly	Arg	Val	Ala	345
Gln	Ile	Arg	Gln	Glu	Ile	Glu	Asn	Ser	Asp	Ser	Asp	Tyr	Asp	Arg	360
Glu	Lys	Leu	Gln	Glu	Arg	Leu	Ala	Lys	Leu	Ala	Gly	Gly	Val	Ala	375
Val	Ile	Lys	Ala	Gly	Ala	Ala	Thr	Glu	Val	Glu	Leu	Lys	Glu	Arg	390
Lys	His	Arg	Ile	Glu	Asp	Ala	Val	Arg	Asn	Ala	Lys	Ala	Ala	Val	405
Glu	Glu	Gly	Ile	Val	Ala	Gly	Gly	Gly	Val	Thr	Leu	Leu	Gln	Ala	420
Ala	Pro	Thr	Leu	Asp	Glu	Leu	Lys	Leu	Glu	Gly	Asp	Glu	Ala	Thr	435
Gly	Ala	Asn	Ile	Val	Lys	Val	Ala	Leu	Glu	Ala	Pro	Leu	Lys	Gln	450
Ile	Ala	Phe	Asn	Ser	Gly	Leu	Glu	Pro	Gly	Val	Val	Ala	Glu	Lys	465
Val	Arg	Asn	Leu	Pro	Ala	Gly	His	Gly	Leu	Asn	Ala	Gln	Thr	Gly	480
Val	Lys	Glu	Asp	Leu	Leu	Ala	Ala	Gly	Val	Ala	Asp	Pro	Val	Lys	495
Val	Thr	Arg	Ser	Ala	Leu	Gln	Asn	Ala	Ala	Ser	Ile	Ala	Gly	Leu	510
Phe	Leu	Thr	Thr	Glu	Ala	Val	Val	Ala	Asp	Lys	Pro	Glu	Lys	Glu	525
Lys	Ala	Ser	Val	Pro	Gly	Gly	Gly	Asp	Met	Gly	Gly	Met	Asp	Phe	540

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 333

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: UNKNOWN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Ala	Val	Lys	Val	Gly	Ile	Asn	Gly	Phe	Gly	Arg	Ile	Gly	Arg	Asn	15
Val	Phe	Arg	Ala	Ala	Leu	Lys	Asn	Pro	Asp	Ile	Glu	Val	Val	Ala	30
Val	Asn	Asp	Leu	Thr	Asp	Ala	Asn	Thr	Leu	Ala	His	Leu	Leu	Lys	45
Tyr	Asp	Ser	Val	His	Gly	Arg	Leu	Asp	Ala	Glu	Val	Ser	Val	Asn	60
Gly	Asn	Asn	Leu	Val	Val	Asn	Gly	Lys	Glu	Ile	Ile	Val	Lys	Ala	75
Glu	Arg	Asp	Pro	Glu	Asn	Leu	Ala	Trp	Gly	Glu	Ile	Gly	Val	Asp	90
Ile	Val	Val	Glu	Ser	Thr	Gly	Arg	Phe	Thr	Lys	Arg	Glu	Asp	Ala	105
Ala	Lys	His	Leu	Glu	Ala	Gly	Ala	Lys	Lys	Val	Ile	Ile	Ser	Ala	120
Pro	Ala	Lys	Asn	Glu	Asp	Ile	Thr	Ile	Val	Met	Gly	Val	Asn	Gln	135
Asp	Lys	Tyr	Asp	Pro	Lys	Ala	His	His	Val	Ile	Ser	Asn	Ala	Ser	150
Cys	Thr	Thr	Asn	Cys	Leu	Ala	Pro	Phe	Ala	Lys	Val	Leu	His	Glu	165
Gln	Phe	Gly	Ile	Val	Arg	Gly	Met	Met	Thr	Thr	Val	His	Ser	Tyr	180
Thr	Asn	Asp	Gln	Arg	Ile	Leu	Asp	Leu	Pro	His	Lys	Asp	Leu	Arg	195
Arg	Ala	Arg	Ala	Ala	Ala	Glu	Ser	Ile	Ile	Pro	Thr	Thr	Thr	Gly	210
Ala	Ala	Lys	Ala	Val	Ala	Leu	Val	Leu	Pro	Glu	Leu	Lys	Gly	Lys	225
Leu	Asn	Gly	Met	Ala	Met	Arg	Val	Pro	Thr	Pro	Asn	Val	Ser	Val	240
Val	Asp	Leu	Val	Ala	Glu	Leu	Glu	Lys	Glu	Val	Thr	Val	Glu	Glu	255
Val	Asn	Ala	Ala	Leu	Lys	Ala	Ala	Ala	Glu	Gly	Glu	Leu	Lys	Gly	270
Ile	Leu	Ala	Tyr	Ser	Glu	Glu	Pro	Leu	Val	Ser	Arg	Asp	Tyr	Asn	285
Gly	Ser	Thr	Val	Ser	Ser	Thr	Ile	Asp	Ala	Leu	Ser	Thr	Met	Val	300
Ile	Asp	Gly	Lys	Met	Val	Lys	Val	Val	Ser	Trp	Tyr	Asp	Asn	Glu	315
Thr	Gly	Tyr	Ser	His	Arg	Val	Val	Asp	Leu	Ala	Ala	Tyr	Ile	Ala	330
Ser	Lys	Gly													

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 332

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: UNKNOWN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Val	Lys	Val	Gly	Val	Asn	Gly	Phe	Gly	Arg	Ile	Gly	Arg	Leu	Val	15
Thr	Arg	Ala	Ala	Phe	Ser	Cys	Asp	Lys	Val	Asp	Ile	Val	Ala	Ile	30

Asn Asp Pro Phe Ile Asp Leu Asn Tyr Met Val Tyr Met Phe Gln 45
 Tyr Asp Ser Thr His Gly Lys Phe Asn Gly Thr Val Lys Ala Glu 60
 Asn Gly Lys Leu Val Ile Asn Gly Lys Pro Ile Thr Ile Phe Gln 75
 Glu Arg Asp Pro Val Lys Ile Lys Trp Gly Asp Ala Gly Ala Glu 90
 Tyr Val Val Glu Ser Thr Gly Val Phe Thr Thr Met Glu Lys Ala 105
 Gly Ala His Leu Lys Gly Gly Ala Lys Arg Val Ile Ile Ser Ala 120
 Pro Ser Ala Asp Ala Pro Met Phe Val Met Gly Val Asn His Glu 135
 Lys Tyr Asp Asn Ser Leu Lys Ile Val Ser Asn Ala Ser Cys Thr 150
 Thr Asn Cys Leu Ala Pro Leu Ala Lys Val Ile His Asp Asn Phe 165
 Gly Ile Val Glu Gly Leu Met Thr Thr Val His Ala Ile Thr Ala 180
 Thr Gln Lys Thr Val Asp Gly Pro Ser Gly Lys Leu Trp Arg Asp 195
 Gly Arg Gly Ala Ala Gln Asn Ile Ile Pro Ala Ser Thr Gly Ala 210
 Ala Lys Ala Val Gly Lys Val Ile Pro Glu Leu Asn Gly Lys Leu 225
 Thr Gly Met Ala Phe Arg Val Pro Thr Pro Asn Val Ser Val Val 240
 Asp Leu Thr Cys Arg Leu Glu Lys Pro Ala Lys Tyr Asp Asp Ile 255
 Lys Lys Val Val Lys Gln Ala Ala Glu Gly Pro Leu Lys Gly Ile 270
 Leu Gly Tyr Thr Glu Asp Gln Val Val Ser Cys Asp Phe Asn Ser 285
 Asn Ser His Ser Ser Thr Phe Asp Ala Gly Ile Ala Leu 300
 Asn Asp Asn Ile Val Lys Leu Ile Ser Trp Tyr Asp Asn Glu Tyr 315
 Gly Tyr Ser Asn Arg Val Val Asp Leu Met Ala Tyr Met Ala Ser 330
 Lys Glu

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 573

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: UNKNOWN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Leu Arg Leu Pro Thr Val Phe Arg Gln Met Arg Pro Val Ser 15
 Arg Val Leu Ala Pro His Leu Thr Arg Ala Tyr Ala Lys Asp Val 30
 Lys Phe Gly Ala Asp Ala Arg Ala Leu Met Leu Gln Gly Val Asp 45
 Leu Leu Ala Asp Ala Val Ala Val Thr Met Gly Pro Lys Gly Arg 60
 Thr Val Ile Ile Glu Gln Ser Trp Gly Ser Pro Lys Val Thr Lys 75
 Asp Gly Val Thr Val Ala Lys Ser Ile Asp Leu Lys Asp Lys Tyr 90
 Lys Asn Ile Gly Ala Lys Leu Val Gln Asp Val Ala Asn Asn Thr 105
 Asn Glu Glu Ala Gly Asp Gly Thr Thr Thr Val Leu Ala 120
 Arg Ser Ile Ala Lys Glu Gly Phe Glu Lys Ile Ser Lys Gly Ala 135
 Asn Pro Val Glu Ile Arg Arg Gly Val Met Leu Ala Val Asp Ala 150
 Val Ile Ala Glu Leu Lys Lys Gln Ser Lys Pro Val Thr Thr Pro 165
 Glu Glu Ile Ala Gln Val Ala Thr Ile Ser Ala Asn Gly Asp Lys 180
 Glu Ile Gly Asn Ile Ile Ser Asp Ala Met Lys Lys Val Gly Arg 195
 Lys Gly Val Ile Thr Val Lys Asp Gly Lys Thr Leu Asn Asp Glu 210
 Leu Glu Ile Ile Glu Gly Met Lys Phe Asp Arg Gly Tyr Ile Ser 225
 Pro Tyr Phe Ile Asn Thr Ser Lys Gly Gln Lys Cys Glu Phe Gln 240
 Asp Ala Tyr Val Leu Leu Ser Glu Lys Lys Ile Ser Ser Ile Gln 255
 Ser Ile Val Pro Ala Leu Glu Ile Ala Asn Ala His Arg Lys Pro 270
 Leu Val Ile Ile Ala Glu Asp Val Asp Gly Glu Ala Leu Ser Thr 285
 Leu Val Leu Asn Arg Leu Lys Val Gly Leu Gln Val Val Ala Val 300
 Lys Ala Pro Gly Phe Gly Asp Asn Arg Lys Asn Gln Leu Lys Asp 315
 Met Ala Ile Ala Thr Gly Gly Ala Val Phe Gly Glu Glu Gly Leu 330
 Thr Leu Asn Leu Glu Asp Val Gln Pro His Asp Leu Gly Lys Val 345
 Gly Glu Val Ile Val Thr Lys Asp Ala Met Leu Leu Lys Gly 360
 Lys Gly Asp Lys Ala Gln Ile Glu Lys Arg Ile Gln Glu Ile Ile 375
 Glu Gln Leu Asp Val Thr Thr Ser Glu Tyr Glu Lys Glu Lys Leu 390
 Asn Glu Arg Leu Ala Lys Leu Ser Asp Gly Val Ala Val Leu Lys 405

Val	Gly	Gly	Thr	Ser	Asp	Val	Glu	Val	Asn	Glu	Lys	Lys	Asp	Arg	420
Val	Thr	Asp	Ala	Leu	Asn	Ala	Thr	Arg	Ala	Ala	Val	Glu	Glu	Gly	435
Ile	Val	Leu	Gly	Gly	Cys	Ala	Leu	Leu	Arg	Cys	Ile	Pro	Ala		450
Leu	Asp	Ser	Leu	Thr	Pro	Ala	Asn	Glu	Asp	Gln	Lys	Ile	Gly	Ile	465
Glu	Il	Il	Lys	Arg	Thr	Leu	Lys	Ile	Pro	Ala	Met	Thr	Ile	Ala	480
Lys	Asn	Ala	Gly	Val	Glu	Gly	Ser	Leu	Ile	Val	Glu	Lys	Ile	Met	495
Gln	Ser	Ser	Ser	Glu	Val	Gly	Tyr	Asp	Ala	Met	Ala	Gly	Asp	Phe	510
Val	Asn	Met	Val	Glu	Lys	Gly	Ile	Ile	Asp	Pro	Thr	Lys	Val	Val	525
Arg	Thr	Ala	Leu	Leu	Asp	Ala	Ala	Gly	Val	Ala	Ser	Leu	Leu	Thr	540
Thr	Ala	Glu	Val	Val	Thr	Glu	Ile	Pro	Lys	Glu	Glu	Lys	Asp		555
Pro	Gly	Met	Gly	Ala	Met	Gly	Gly	Met	Gly	Gly	Gly	Met	Gly	Gly	570
Gly	Met	Phe													

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 547

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: UNKNOWN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Ala	Lys	Asp	Val	Lys	Phe	Gly	Ala	Asp	Ala	Arg	Ala	Leu	Met	Leu	15
Gln	Gly	Val	Asp	Leu	Leu	Ala	Asp	Ala	Val	Ala	Val	Thr	Met	Gly	30
Pro	Lys	Gly	Arg	Thr	Val	Ile	Ile	Glu	Gln	Ser	Trp	Gly	Ser	Pro	45
Lys	Val	Thr	Lys	Asp	Gly	Val	Thr	Val	Ala	Lys	Ser	Ile	Asp	Leu	60
Lys	Asp	Lys	Tyr	Lys	Asn	Ile	Gly	Ala	Lys	Leu	Val	Gln	Asp	Val	75
Ala	Asn	Asn	Thr	Asn	Glu	Ala	Gly	Asp	Gly	Thr	Thr	Thr	Ala		90
Thr	Val	Leu	Ala	Arg	Ser	Ile	Ala	Lys	Glu	Gly	Phe	Glu	Lys	Ile	105
Ser	Lys	Gly	Ala	Asn	Pro	Val	Glu	Ile	Arg	Arg	Gly	Val	Met	Leu	120
Ala	Val	Asp	Ala	Val	Ile	Ala	Glu	Leu	Lys	Lys	Gln	Ser	Lys	Pro	135
Val	Thr	Thr	Pro	Glu	Glu	Ile	Ala	Gln	Val	Ala	Thr	Ile	Ser	Ala	150
Asn	Gly	Asp	Lys	Asp	Ile	Gly	Asn	Ile	Ile	Ser	Asp	Ala	Met	Lys	165
Lys	Val	Gly	Arg	Lys	Gly	Val	Ile	Thr	Val	Lys	Asp	Gly	Lys	Thr	180
Leu	Asn	Asp	Glu	Leu	Glu	Ile	Ile	Glu	Gly	Met	Lys	Phe	Asp	Arg	195
Gly	Tyr	Ile	Ser	Pro	Tyr	Phe	Ile	Asn	Thr	Ser	Lys	Gly	Gln	Lys	210
Cys	Glu	Phe	Gln	Asp	Ala	Tyr	Val	Leu	Leu	Ser	Glu	Lys	Lys	Ile	225
Ser	Ser	Val	Gln	Ser	Ile	Val	Pro	Ala	Leu	Glu	Ile	Ala	Asn	Ala	240
His	Arg	Lys	Pro	Leu	Val	Ile	Ile	Ala	Glu	Asp	Val	Asp	Gly	Glu	255
Ala	Leu	Ser	Thr	Leu	Val	Leu	Asn	Arg	Leu	Lys	Val	Gly	Leu	Gln	270
Val	Val	Ala	Val	Lys	Ala	Pro	Gly	Phe	Gly	Asp	Asn	Arg	Lys	Asn	285
Gln	Leu	Lys	Asp	Met	Ala	Ile	Ala	Thr	Gly	Gly	Ala	Val	Phe	Gly	300
Glu	Glu	Gly	Leu	Asn	Leu	Asn	Leu	Glu	Asp	Val	Gln	Ala	His	Asp	315
Leu	Gly	Lys	Val	Gly	Glu	Val	Ile	Val	Thr	Lys	Asp	Asp	Ala	Met	330
Leu	Leu	Lys	Gly	Lys	Gly	Asp	Lys	Ala	His	Ile	Glu	Lys	Arg	Ile	345
Gln	Glu	Ile	Thr	Glu	Gln	Leu	Asp	Ile	Thr	Thr	Ser	Glu	Tyr	Glu	360
Lys	Glu	Lys	Leu	Asn	Glu	Arg	Leu	Ala	Lys	Leu	Ser	Asp	Gly	Val	375
Ala	Val	Leu	Lys	Val	Gly	Gly	Thr	Ser	Asp	Val	Glu	Val	Asn	Glu	390
Lys	Lys	Asp	Arg	Val	Thr	Asp	Ala	Leu	Asn	Ala	Thr	Arg	Ala	Ala	405
Val	Glu	Glu	Gly	Ile	Val	Leu	Gly	Gly	Cys	Ala	Leu	Leu	Arg		420
Cys	Ile	Pro	Ala	Leu	Asp	Ser	Leu	Lys	Pro	Ala	Asn	Glu	Asp	Gln	435
Lys	Ile	Gly	Ile	Glu	Ile	Ile	Lys	Arg	Ala	Leu	Lys	Ile	Pro	Ala	450
Met	Thr	Ile	Ala	Lys	Asn	Ala	Gly	Val	Glu	Gly	Ser	Leu	Ile	Val	465
Glu	Lys	Ile	Leu	Gln	Ser	Ser	Ser	Glu	Val	Gly	Tyr	Asp	Ala	Met	480
Leu	Gly	Asp	Phe	Val	Asn	Met	Val	Glu	Lys	Gly	Ile	Ile	Asp	Pro	495
Thr	Lys	Val	Val	Arg	Thr	Ala	Leu	Leu	Asp	Ala	Ala	Gly	Val	Ala	510
Ser	Leu	Leu	Thr	Thr	Ala	Glu	Ala	Val	Val	Thr	Glu	Ile	Pro	Lys	525

Glu Glu Lys Asp Pro Gly Met Gly Ala Met Gly Gly Met Gly Gly 540
 Gly Met Gly Gly Gly Met Phe

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 555

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: UNKNOWN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Ala	Pro	His	Leu	Thr	Arg	Ala	Tyr	Ala	Lys	Asp	Val	Lys	Phe	Gly	15
Ala	Asp	Ala	Arg	Ala	Leu	Met	Leu	Gln	Gly	Val	Asp	Leu	Leu	Ala	30
Asp	Ala	Val	Ala	Val	Thr	Met	Gly	Pro	Lys	Gly	Arg	Thr	Val	Ile	45
Ile	Glu	Gln	Ser	Trp	Gly	Ser	Pro	Lys	Val	Thr	Lys	Asp	Gly	Val	60
Thr	Val	Ala	Lys	Ser	Ile	Asp	Leu	Lys	Asp	Lys	Tyr	Lys	Asn	Ile	75
Gly	Ala	Lys	Leu	Val	Gln	Asp	Val	Ala	Asn	Asn	Thr	Asn	Glu	Glu	90
Ala	Gly	Asp	Gly	Thr	Thr	Thr	Ala	Thr	Val	Leu	Ala	Arg	Ser	Ile	105
Ala	Lys	Glu	Gly	Phe	Glu	Lys	Ile	Ser	Lys	Gly	Ala	Asn	Pro	Val	120
Glu	Ile	Arg	Arg	Gly	Val	Met	Leu	Ala	Val	Asp	Ala	Val	Ile	Ala	135
Glu	Leu	Lys	Lys	Gln	Ser	Lys	Pro	Val	Thr	Thr	Pro	Glu	Glu	Ile	150
Ala	Gln	Val	Ala	Thr	Ile	Ser	Ala	Asn	Gly	Asp	Lys	Asp	Ile	Gly	165
Asn	Ile	Ile	Ser	Asp	Ala	Met	Lys	Lys	Val	Gly	Arg	Lys	Gly	Val	180
Ile	Thr	Val	Lys	Asp	Gly	Lys	Thr	Leu	Asn	Asp	Glu	Leu	Glu	Ile	195
Ile	Glu	Gly	Met	Lys	Phe	Asp	Arg	Gly	Tyr	Ile	Ser	Pro	Tyr	Phe	210
Ile	Asn	Thr	Ser	Lys	Gly	Gln	Lys	Cys	Glu	Phe	Gln	Asp	Ala	Tyr	225
Val	Leu	Leu	Ser	Glu	Lys	Lys	Phe	Ser	Ser	Val	Gln	Ser	Ile	Val	240
Pro	Ala	Leu	Glu	Ile	Ala	Asn	Ala	His	Arg	Lys	Pro	Leu	Val	Ile	255
Ile	Ala	Glu	Asp	Val	Asp	Gly	Glu	Ala	Leu	Ser	Thr	Leu	Val	Leu	270
Asn	Arg	Leu	Lys	Val	Gly	Leu	Gln	Val	Val	Ala	Val	Lys	Ala	Pro	285
Gly	Phe	Gly	Asp	Asn	Arg	Lys	Asn	Gln	Leu	Lys	Asp	Met	Ala	Ile	300
Ala	Thr	Gly	Gly	Ala	Val	Phe	Gly	Glu	Glu	Gly	Leu	Asn	Leu	Asn	315
Leu	Glu	Asp	Val	Gln	Ala	His	Asp	Leu	Gly	Lys	Val	Gly	Glu	Val	330
Ile	Val	Thr	Lys	Asp	Asp	Ala	Met	Leu	Leu	Lys	Gly	Lys	Gly	Asp	345
Lys	Ala	His	Ile	Glu	Lys	Arg	Ile	Gln	Glu	Ile	Thr	Glu	Gln	Leu	360
Asp	Ile	Thr	Thr	Ser	Glu	Tyr	Glu	Lys	Glu	Lys	Leu	Asn	Glu	Arg	375
Leu	Ala	Lys	Leu	Ser	Asp	Gly	Val	Ala	Val	Leu	Lys	Val	Gly	Gly	390
Thr	Ser	Asp	Val	Glu	Val	Asn	Glu	Lys	Lys	Asp	Arg	Val	Thr	Asp	405
Ala	Leu	Asn	Ala	Thr	Arg	Ala	Ala	Val	Glu	Glu	Gly	Ile	Val	Leu	420
Gly	Gly	Gly	Cys	Ala	Leu	Leu	Arg	Cys	Ile	Pro	Ala	Leu	Asp	Ser	435
Leu	Lys	Pro	Ala	Asn	Glu	Asp	Gln	Lys	Ile	Gly	Ile	Glu	Ile	Ile	450
Lys	Arg	Ala	Leu	Lys	Ile	Pro	Ala	Met	Thr	Ile	Ala	Lys	Asn	Ala	465
Gly	Val	Glu	Gly	Ser	Leu	Ile	Val	Glu	Lys	Ile	Leu	Gln	Ser	Ser	480
Ser	Glu	Val	Gly	Tyr	Asp	Ala	Met	Leu	Gly	Asp	Phe	Val	Asn	Met	495
Val	Glu	Lys	Gly	Ile	Ile	Asp	Pro	Thr	Lys	Val	Val	Arg	Thr	Ala	510
Leu	Leu	Asp	Ala	Ala	Gly	Val	Ala	Ser	Leu	Leu	Thr	Thr	Ala	Glu	525
Ala	Val	Val	Thr	Glu	Ile	Pro	Lys	Glu	Glu	Lys	Asp	Pro	Gly	Met	540
Gly	Ala	Met	Gly	Gly	Met	Gly	Gly	Gly	Gly	Met	Gly	Gly	Met	Phe	555